$$E = R^{-6}/(R^{-6} + R_o^{-6})$$

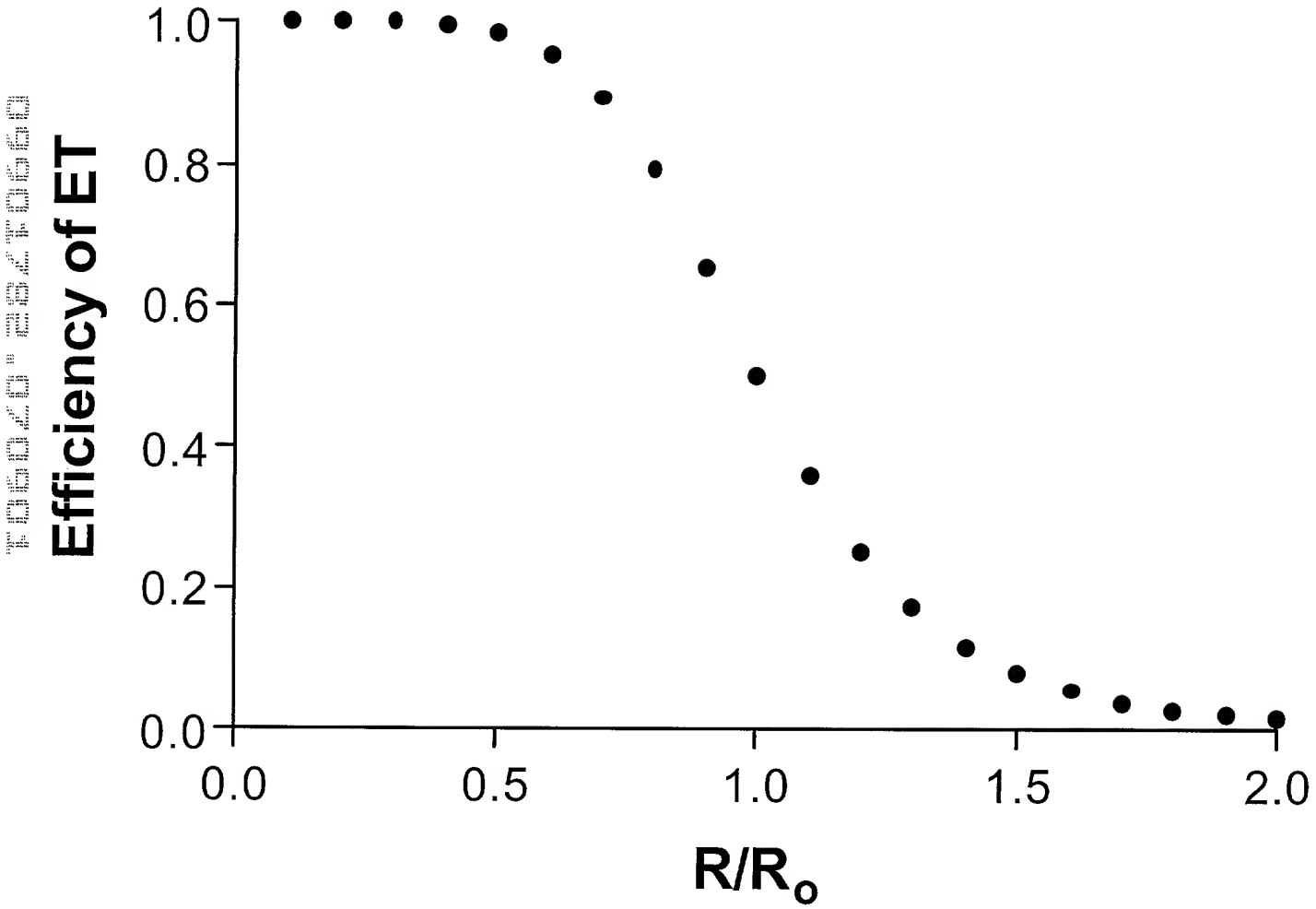


FIG. 1

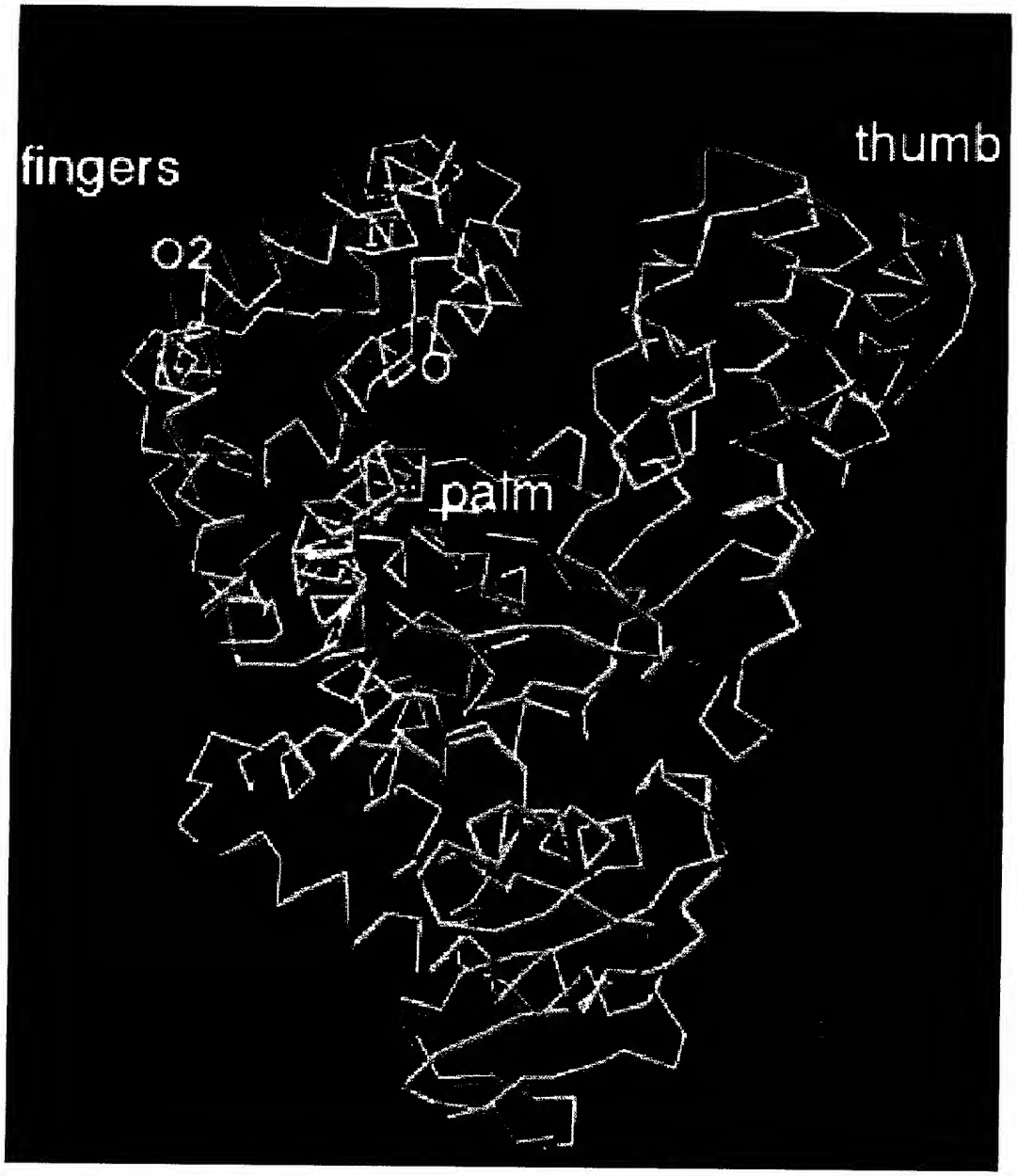


FIG. 2

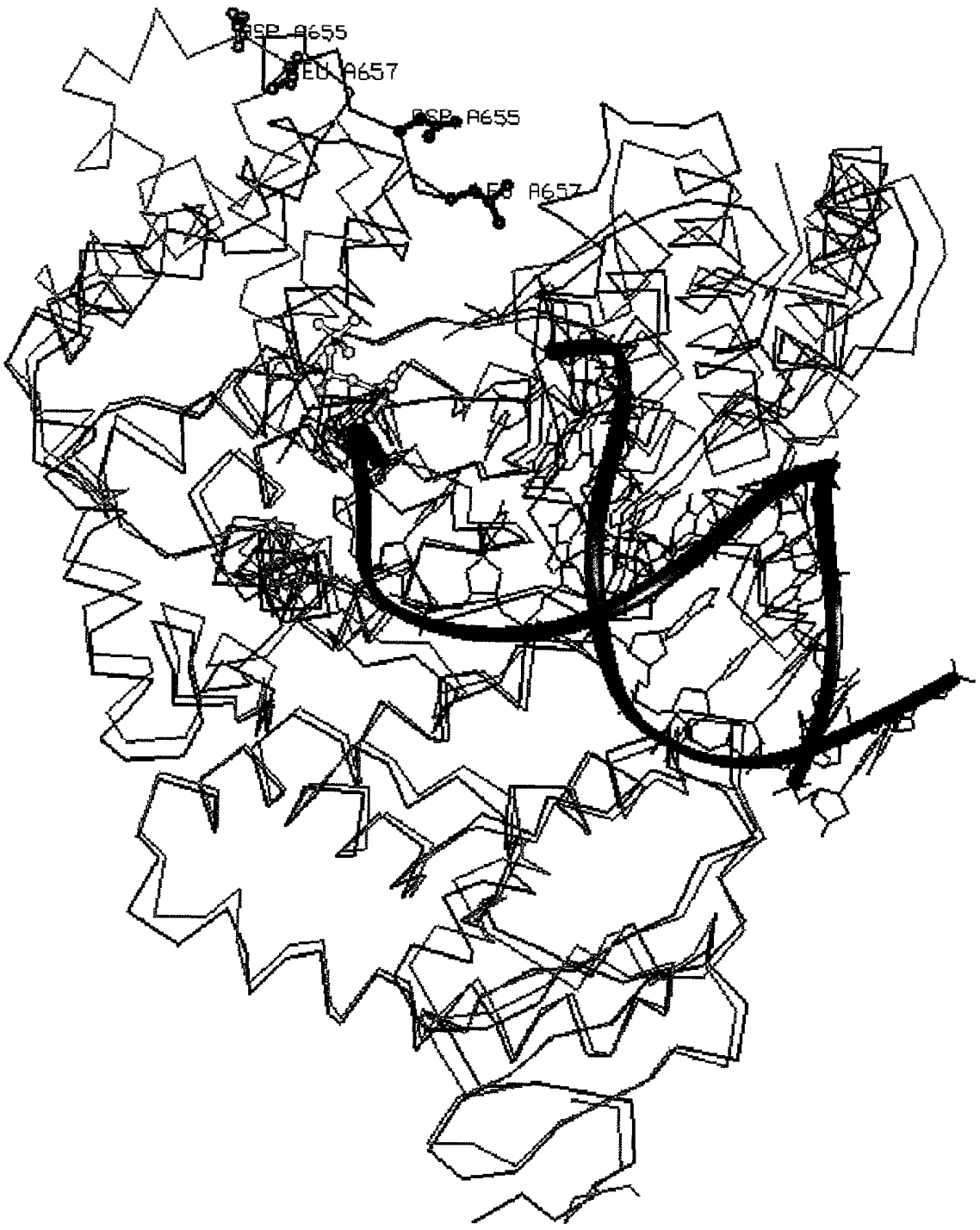


FIG. 3A

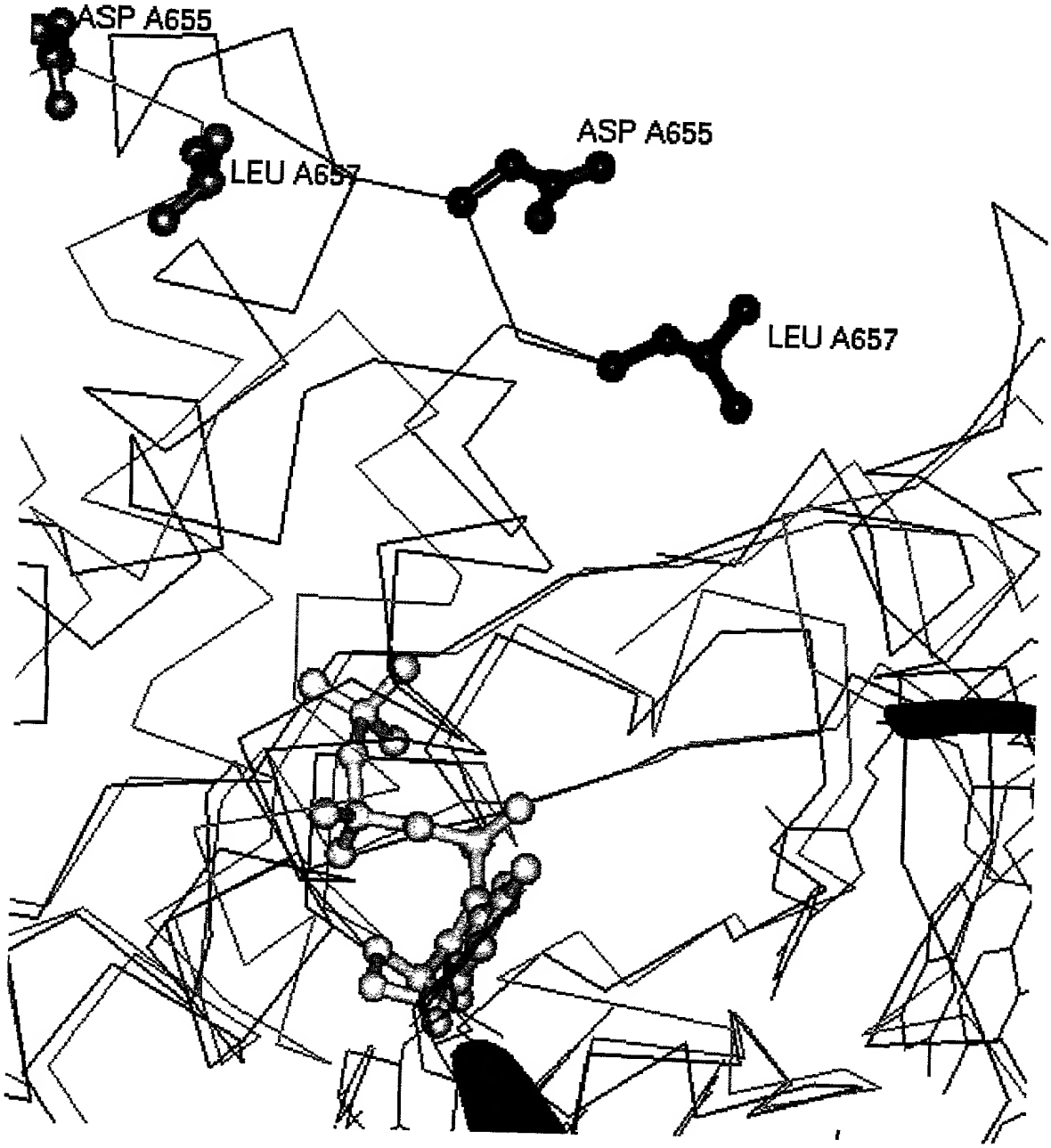


FIG. 3B

FIG. 3c

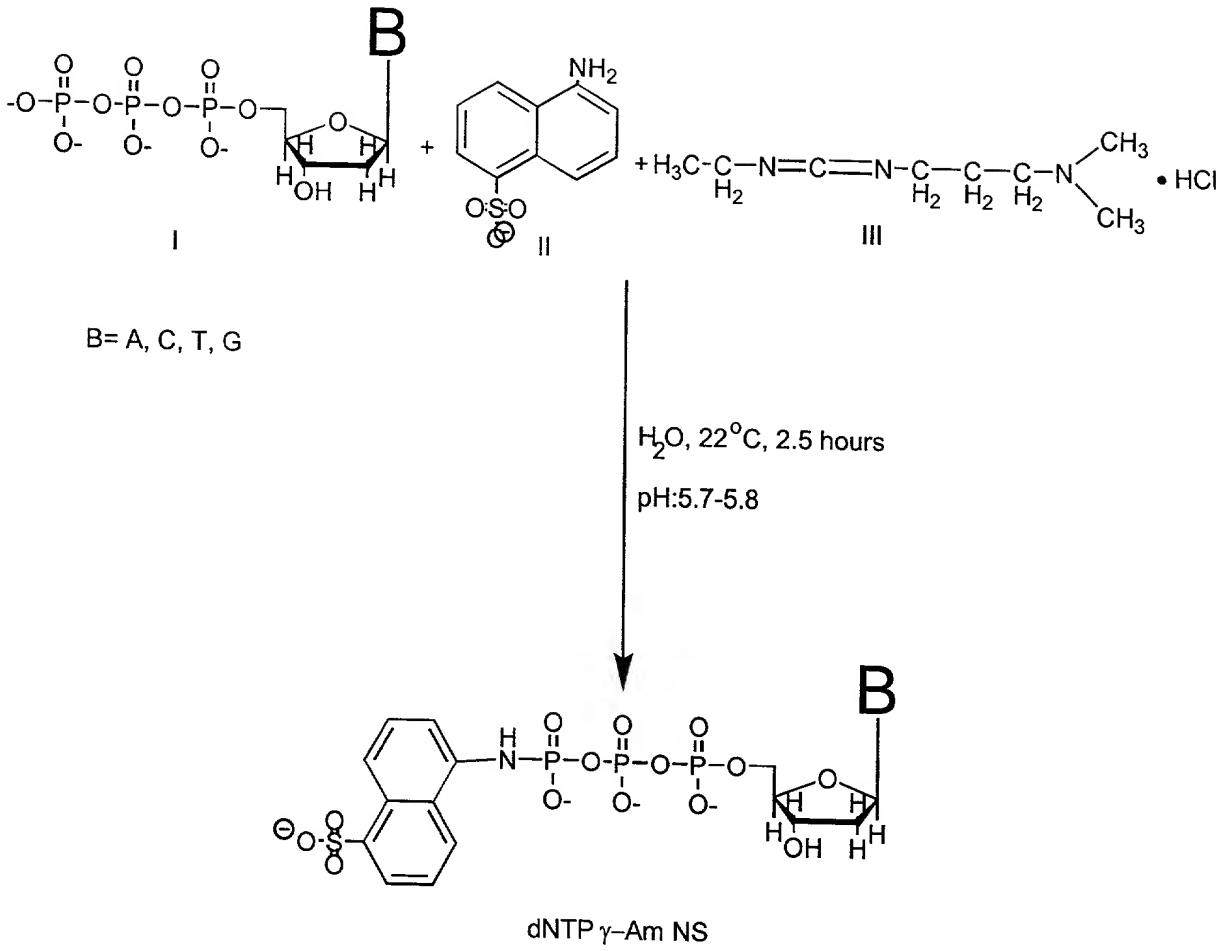

B
NH2
+ H3C-C-N=C=N-C-C-C-N
H2
H2 H2 H2
CH3
CH3
• HCl
I
II
III
B= A, C, T, G
H2O, 22°C, 2.5 hours
pH:5.7-5.8
B
dNTP γ–Am NS

FIG. 4

Primer Strand:		
	TOP 5'	GGT ACT AAG CGG CCG CAT G 3'
Template Strands:		
	BOT-T 3'	CCA TGA TTC GCC GGC GTA CTC 5'
	BOT-C 3'	CCA TGA TTC GCC GGC GTA CCC 5'
	BOT-G 3'	CCA TGA TTC GCC GGC GTA CGC 5'
	BOT-A 3'	CCA TGA TTC GCC GGC GTA CAC 5'
	BOT-3T 3'	CCA TGA TTC GCC GGC GTA CTT TC 5'
	BOT-Sau 3'	CCA TGA TTC GCC GGC GTA CCT AG 5'

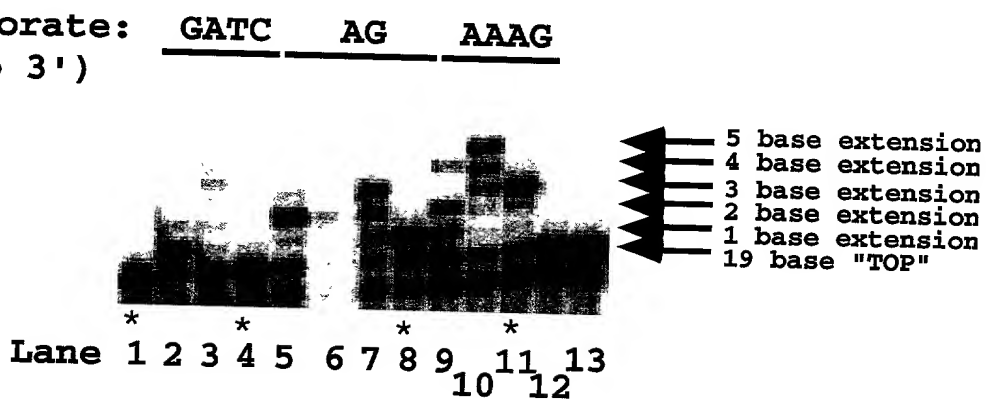


FIG. 5

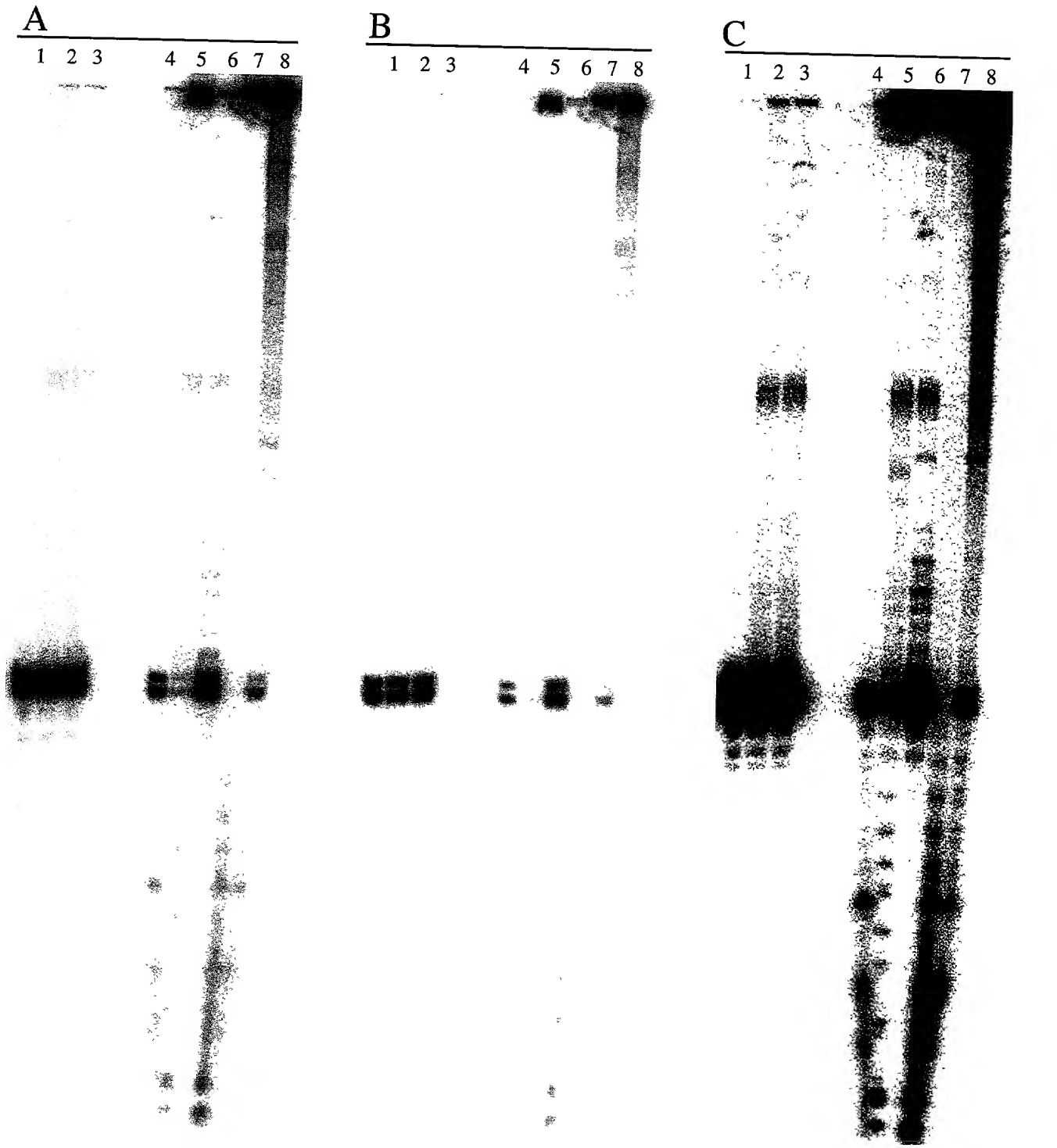


FIG. 6

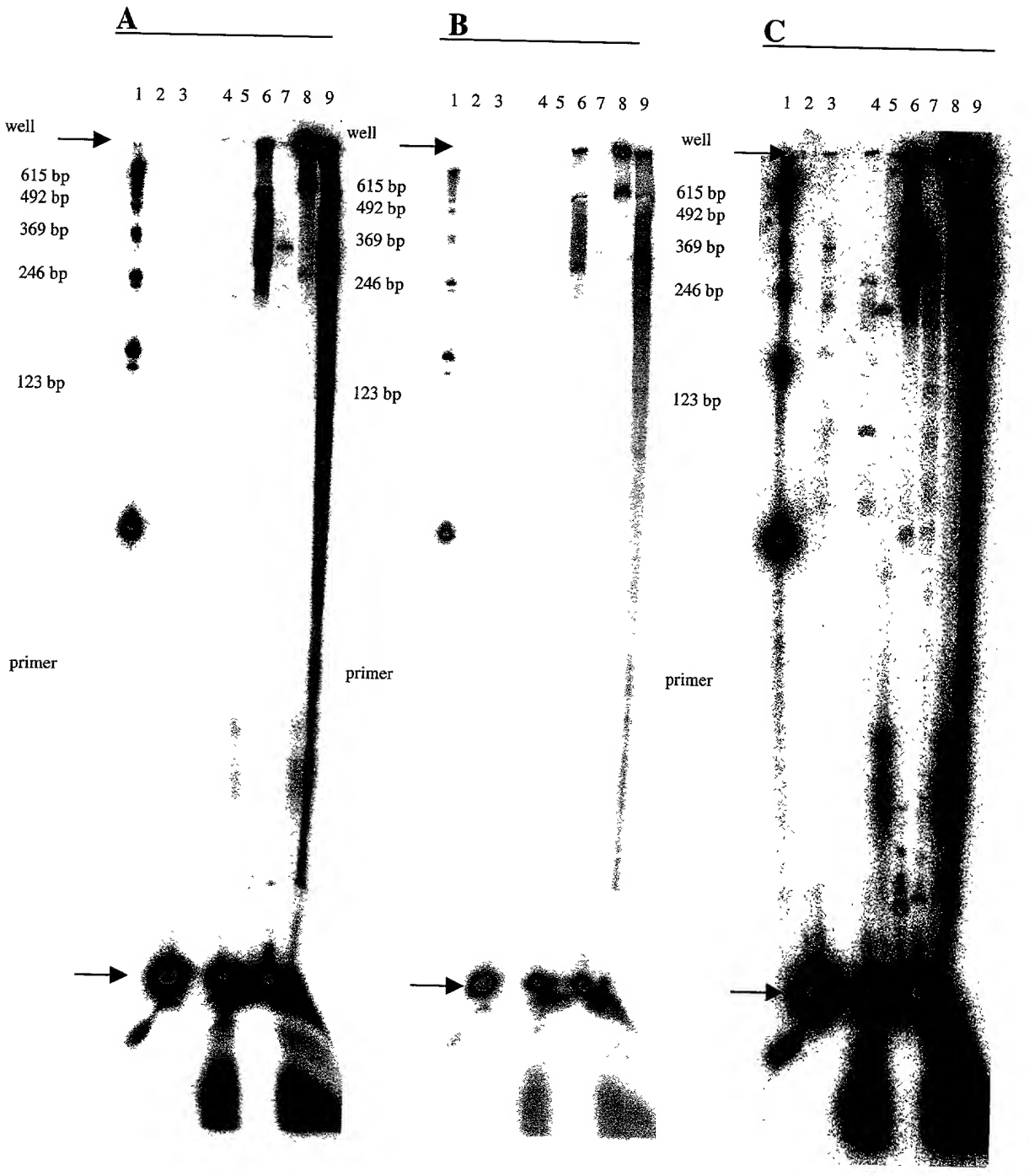


FIG. 7

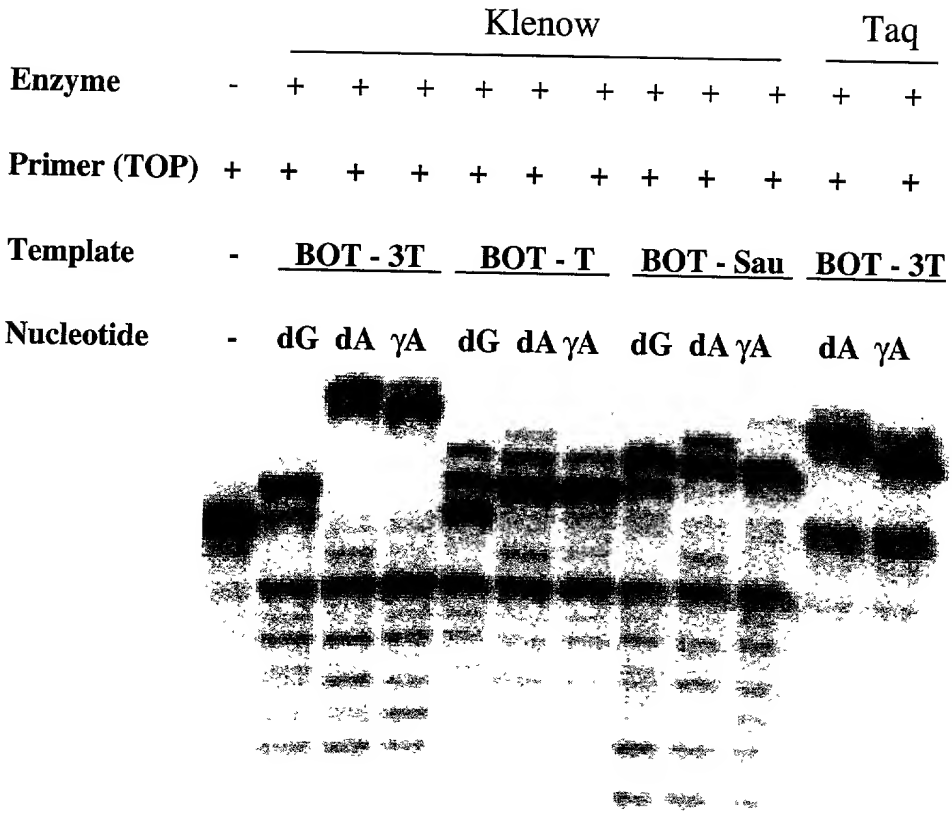

Klenow
Taq
Enzyme - + + + + + + + + + + +
Primer (TOP) + + + + + + + + + + + +
Template - BOT - 3T BOT - T BOT - Sau BOT - 3T
Nucleotide - dG dA γA dG dA γA dG dA γA dA γA

FIG. 8

Pfu Primer Extension Assays

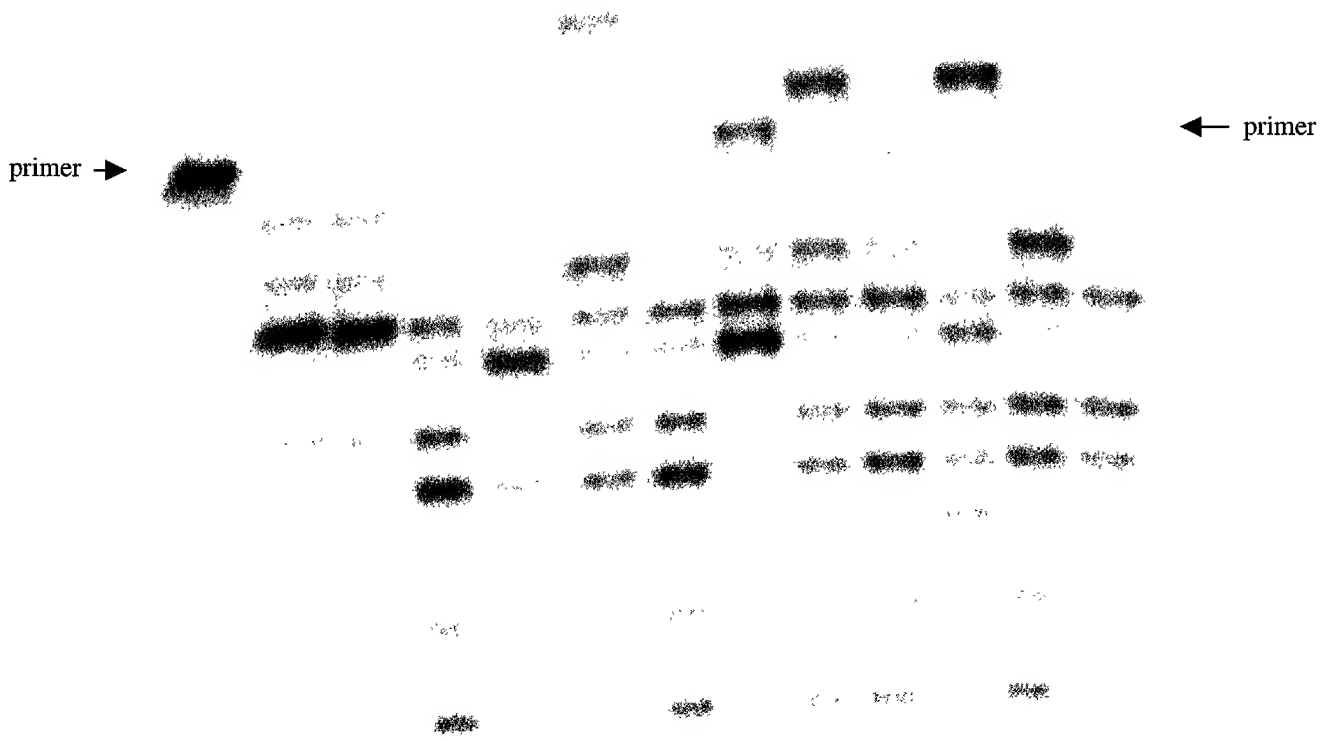


Fig. 9

- Primer Strand:
  Top 5′ GGT ACT AAG CGG CCG CAT G 3′

- Template Strands:
  3T 3′ CCA TGA TTC GCC GGC GTA CTT TC 5′
  Sau 3′ CCA TGA TTC GCC GGC GTA CCT AG 5′

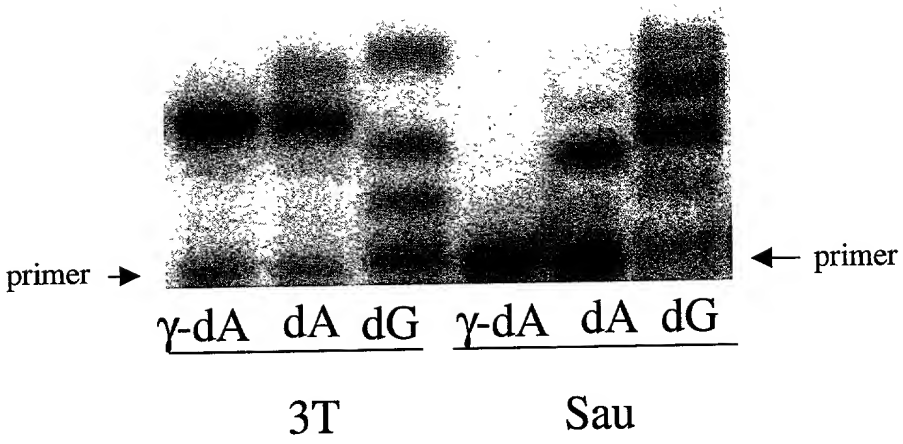


FIG 10

Primer Strand:

Top 5′ GGT ACT AAG CGG CCG CAT G 3′

Template Strands:

BOT-3T 3′ CCA TGA TTC GCC GGC GTA CTT TC 5′

BOT-Sau 3′ CCA TGA TTC GCC GGC GTA CCT AG 5′

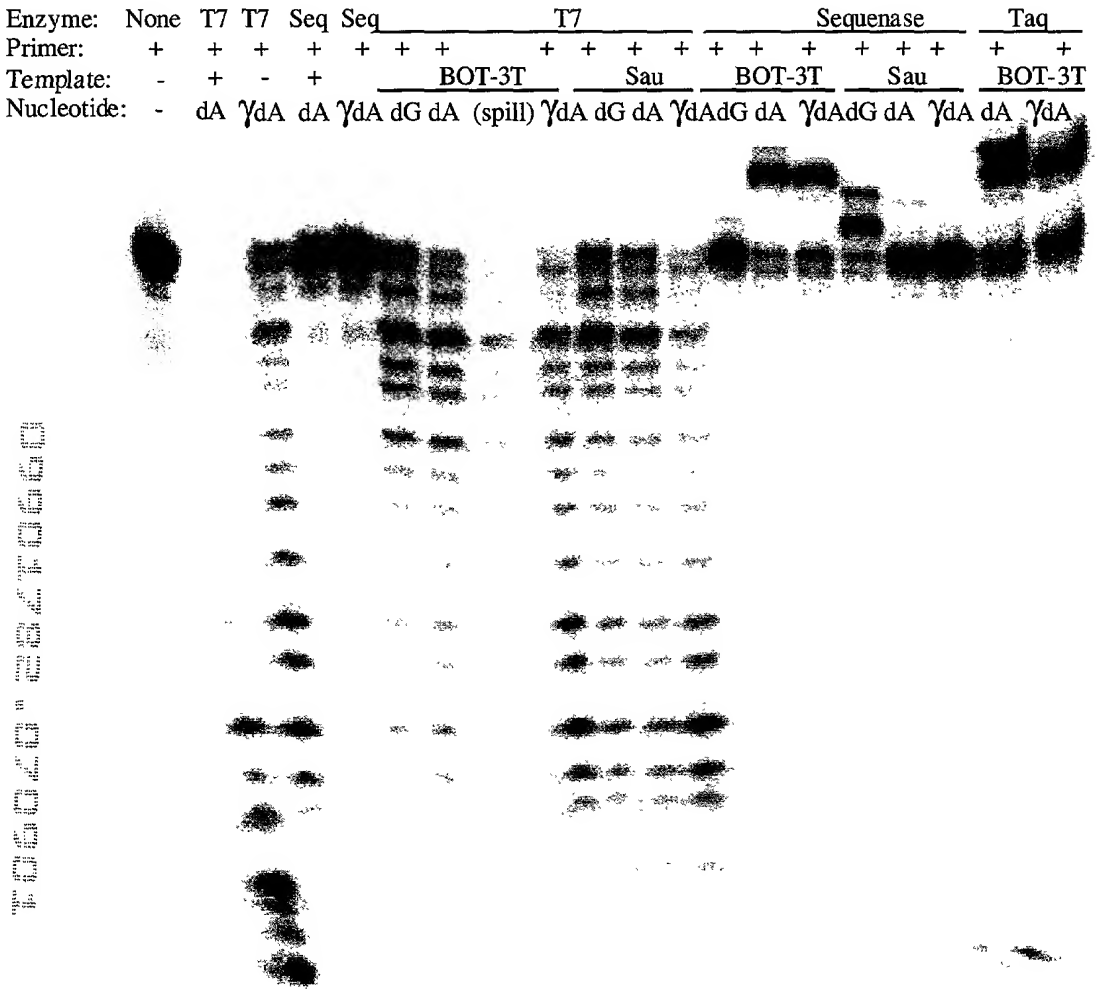
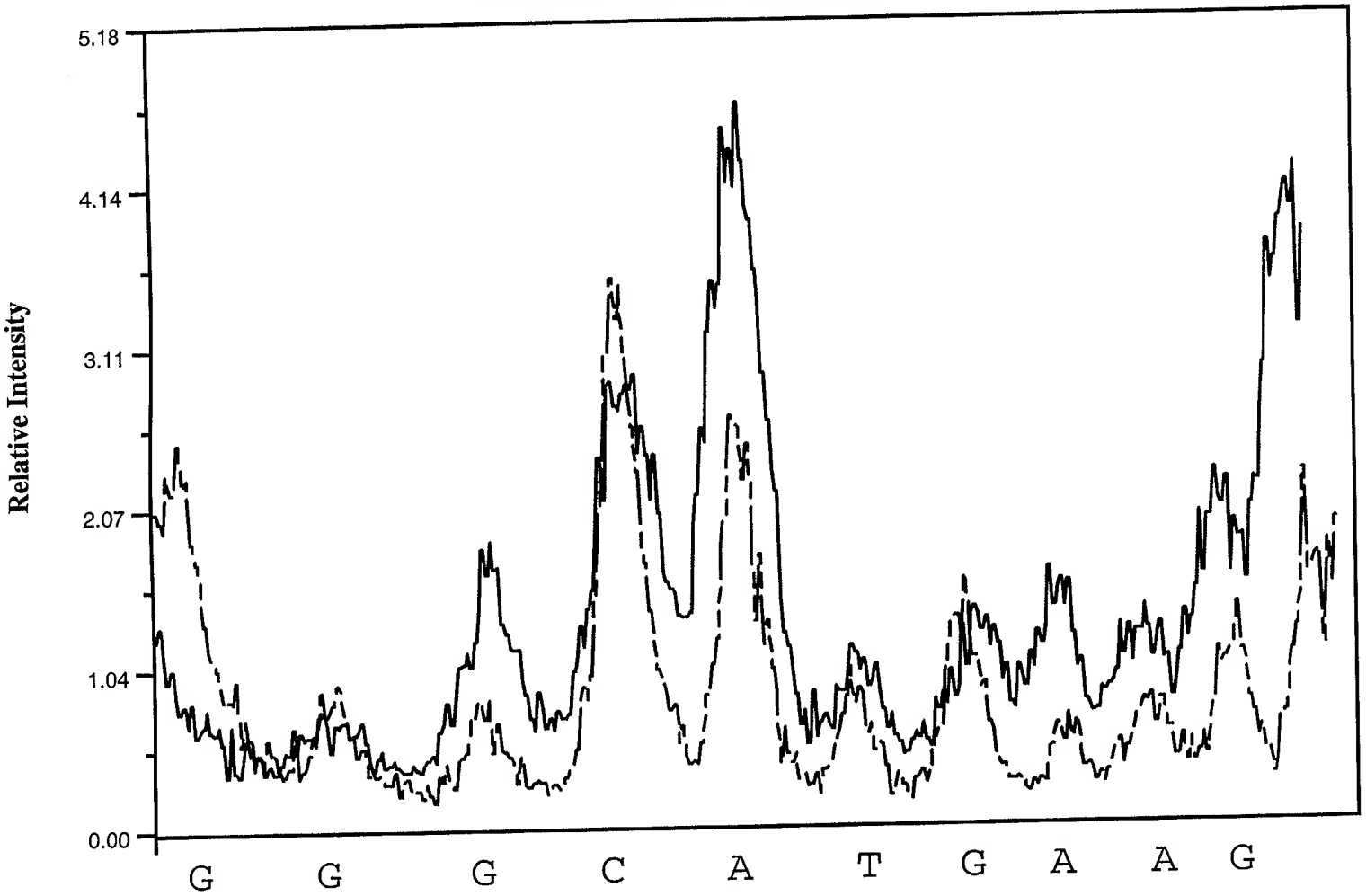


FIG. 11



Signal Intensity and Reaction Kinetics Provide Information Concerning Base Identity. Signal intensities for each nucleotide in the extended DNA strand are used to determine, confirm or support base identity data. The solid green line corresponds to reaction products produced when four natural nucleotides (dATP, dCTP, dGTP and dTTP) are included in the synthesis reaction. The dashed red line corresponds to reaction products produced when proprietary, base-modified nucleotides are included in the reaction. As is clearly demonstrated, sequence context and base modification(s) influence reaction product intensity and/or reaction kinetics, and these identifying patterns are incorporated into proprietary base-calling software to provide a high confidence value for base identity at each sequenced position.

FIG. 12